



OIQE

## RAW SEQUENCE LISTING

DATE: 02/07/2002

PATENT APPLICATION: US/10/056,253

TIME: 09:01:28

Input Set : N:\Crf3\RULE60\10056253.raw

Output Set: N:\CRF3\02072002\J056253.raw

1 <110> APPLICANT: Kapeller Libermann, Rosana  
 2 White, David  
 3 MacBeth, Kyle J.  
 4 <120> TITLE OF INVENTION: 2786, A NOVEL HUMAN AMINOPEPTIDASE  
 5 <130> FILE REFERENCE: 5800-62  
 6 <140> CURRENT APPLICATION NUMBER: 10/056,253  
 7 <141> CURRENT FILING DATE: 2002-01-24  
 9 <150> PRIOR APPLICATION NUMBER: US/09/443,795  
 10 <151> PRIOR FILING DATE: 1999-11-19  
 13 <160> NUMBER OF SEQ ID NOS: 2  
 14 <170> SOFTWARE: FastSEQ for Windows Version 3.0  
 16 <210> SEQ ID NO: 1  
 17 <211> LENGTH: 650  
 18 <212> TYPE: PRT  
 19 <213> ORGANISM: Homo sapiens  
 20 <400> SEQUENCE: 1

21	Met	Ala	Ser	Gly	Glu	His	Ser	Pro	Gly	Ser	Gly	Ala	Ala	Arg	Arg	Pro
22	1				5				10					15		
23	Leu	His	Ser	Ala	Gln	Ala	Val	Asp	Val	Ala	Ser	Ala	Ser	Asn	Phe	Arg
24				20				25						30		
25	Ala	Phe	Glu	Leu	Leu	His	Leu	His	Leu	Asp	Leu	Arg	Ala	Glu	Phe	Gly
26			35				40					45				
27	Pro	Pro	Gly	Pro	Gly	Ala	Gly	Ser	Arg	Gly	Leu	Ser	Gly	Thr	Ala	Val
28		50				55					60					
29	Leu	Asp	Leu	Arg	Cys	Leu	Glu	Pro	Glu	Gly	Ala	Ala	Glu	Leu	Arg	Leu
30	65				70				75					80		
31	Asp	Ser	His	Pro	Cys	Leu	Glu	Val	Thr	Ala	Ala	Ala	Leu	Arg	Arg	Glu
32				85				90						95		
33	Arg	Pro	Gly	Ser	Glu	Glu	Pro	Pro	Ala	Glu	Pro	Val	Ser	Phe	Tyr	Thr
34			100					105						110		
35	Gln	Pro	Phe	Ser	His	Tyr	Gly	Gln	Ala	Leu	Cys	Val	Ser	Phe	Pro	Gln
36			115				120						125			
37	Pro	Cys	Arg	Ala	Ala	Glu	Arg	Leu	Gln	Val	Leu	Leu	Thr	Tyr	Arg	Val
38		130				135					140					
39	Gly	Glu	Gly	Pro	Gly	Val	Cys	Trp	Leu	Ala	Pro	Glu	Gln	Thr	Ala	Gly
40	145				150				155					160		
41	Lys	Lys	Lys	Pro	Phe	Val	Tyr	Thr	Gln	Gly	Gln	Ala	Val	Leu	Asn	Arg
42				165				170						175		
43	Ala	Phe	Phe	Pro	Cys	Phe	Asp	Thr	Pro	Ala	Val	Lys	Tyr	Lys	Tyr	Ser
44			180					185						190		
45	Ala	Leu	Ile	Glu	Val	Pro	Asp	Gly	Phe	Thr	Ala	Val	Met	Ser	Ala	Ser
46		195				200						205				
47	Thr	Trp	Glu	Lys	Arg	Gly	Pro	Asn	Lys	Phe	Phe	Phe	Gln	Met	Cys	Gln

ENTERED

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48          210          215          220
49  Pro Ile Pro Ser Tyr Leu Ile Ala Leu Ala Ile Gly Asp Leu Val Ser
50  225          230          235          240
51  Ala Glu Val Gly Pro Arg Ser Arg Val Trp Ala Glu Pro Cys Leu Ile
52          245          250          255
53  Asp Ala Ala Asn Glu Glu Tyr Asn Gly Val Ile Glu Glu Phe Leu Ala
54          260          265          270
55  Thr Gly Glu Lys Leu Phe Gly Pro Tyr Val Trp Gly Arg Tyr Asp Leu
56          275          280          285
57  Leu Phe Met Pro Pro Ser Phe Pro Phe Gly Gly Met Glu Asn Pro Cys
58          290          295          300
59  Leu Thr Phe Val Thr Pro Cys Leu Leu Ala Gly Asp Arg Ser Leu Ala
60  305          310          315          320
61  Asp Val Ile Ile His Glu Ile Ser His Ser Trp Phe Gly Asn Leu Val
62          325          330          335
63  Thr Asn Ala Asn Trp Gly Glu Phe Trp Leu Asn Glu Gly Phe Thr Met
64          340          345          350
65  Tyr Ala Gln Arg Arg Ile Ser Thr Ile Leu Phe Gly Ala Ala Tyr Thr
66          355          360          365
67  Cys Leu Glu Ala Ala Thr Gly Arg Ala Leu Leu Arg Gln His Met Asp
68          370          375          380
69  Ile Thr Gly Glu Glu Asn Pro Leu Asn Lys Leu Arg Val Lys Ile Glu
70  385          390          395          400
71  Pro Gly Val Asp Pro Asp Asp Thr Tyr Asn Glu Thr Pro Tyr Glu Lys
72          405          410          415
73  Gly Phe Cys Phe Val Ser Tyr Leu Ala His Leu Val Gly Asp Gln Asp
74          420          425          430
75  Gln Phe Asp Ser Phe Leu Lys Ala Tyr Val His Glu Phe Lys Phe Arg
76          435          440          445
77  Ser Ile Leu Ala Asp Asp Phe Leu Asp Phe Tyr Leu Glu Tyr Phe Pro
78          450          455          460
79  Glu Leu Lys Lys Lys Arg Val Asp Ile Ile Pro Gly Phe Glu Phe Asp
80  465          470          475          480
81  Arg Trp Leu Asn Thr Pro Gly Trp Pro Pro Tyr Leu Pro Asp Leu Ser
82          485          490          495
83  Pro Gly Asp Ser Leu Met Lys Pro Ala Glu Glu Leu Ala Gln Leu Trp
84          500          505          510
85  Ala Ala Glu Glu Leu Asp Met Lys Ala Ile Glu Ala Val Ala Ile Ser
86          515          520          525
87  Pro Trp Lys Thr Tyr Gln Leu Val Tyr Phe Leu Asp Lys Ile Leu Gln
88          530          535          540
89  Lys Ser Pro Leu Pro Pro Gly Asn Val Lys Lys Leu Gly Asp Thr Tyr
90  545          550          555          560
91  Pro Ser Ile Ser Asn Ala Arg Asn Ala Glu Leu Arg Leu Arg Trp Gly
92          565          570          575
93  Gln Ile Val Leu Lys Asn Asp His Gln Glu Asp Phe Trp Lys Val Lys
94          580          585          590
95  Glu Phe Leu His Asn Gln Gly Lys Gln Lys Tyr Thr Leu Pro Leu Tyr
96          595          600          605

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```

97      His Ala Met Met Gly Gly Ser Glu Val Ala Gln Thr Leu Ala Lys Glu
98      610      615      620
99      Thr Phe Ala Ser Thr Ala Ser Gln Leu His Ser Asn Val Val Asn Tyr
100     625      630      635      640
101     Val Gln Gln Ile Val Ala Pro Lys Gly Ser
102     645      650
104 <210> SEQ ID NO: 2
105 <211> LENGTH: 2459
106 <212> TYPE: DNA
107 <213> ORGANISM: Homo sapiens
108 <220> FEATURE:
109 <221> NAME/KEY: CDS
110 <222> LOCATION: (62)...(2011)
111 <400> SEQUENCE: 2
112     gcggccgcgt cgacctcccc tcgggttcgc ggcccgcccg gtgagcaacg gctctgcggc      60
113     c atg gcg agc ggc gag cat tcc ccc ggc agc ggc gcg gcc cgg cgg ccg      109
114     Met Ala Ser Gly Glu His Ser Pro Gly Ser Gly Ala Ala Arg Arg Pro
115     1      5      10      15
116     ctg cac tcc gcg cag gct gtg gac gtg gcc tcg gcc tcc aac ttc cgg      157
117     Leu His Ser Ala Gln Ala Val Asp Val Ala Ser Ala Ser Asn Phe Arg
118     20      25      30
119     gcc ttt gag ctg ctg cac ttg cac ctg gac ctg cgg gct gag ttc ggg      205
120     Ala Phe Glu Leu Leu His Leu His Leu Asp Leu Arg Ala Glu Phe Gly
121     35      40      45
122     cct cca ggg ccc ggc gca ggg agc cgg ggg ctg agc ggc acc gcg gtc      253
123     Pro Pro Gly Pro Gly Ala Gly Ser Arg Gly Leu Ser Gly Thr Ala Val
124     50      55      60
125     ctg gac ctg cgc tgc ctg gag ccc gag ggc gcc gcc gag ctg cgg ctg      301
126     Leu Asp Leu Arg Cys Leu Glu Pro Glu Gly Ala Ala Glu Leu Arg Leu
127     65      70      75      80
128     gac tcg cac ccg tgc ctg gag gtg acg gcg gcg gcg ctg cgg cgg gag      349
129     Asp Ser His Pro Cys Leu Glu Val Thr Ala Ala Ala Leu Arg Arg Glu
130     85      90      95
131     cgg ccc ggc tcg gag gag ccg cct gcg gag ccc gtg agc ttc tac acg      397
132     Arg Pro Gly Ser Glu Glu Pro Pro Ala Glu Pro Val Ser Phe Tyr Thr
133     100      105      110
134     cag ccc ttc tcg cac tat ggc cag gcc ctg tgc gtg tcc ttc ccg cag      445
135     Gln Pro Phe Ser His Tyr Gly Gln Ala Leu Cys Val Ser Phe Pro Gln
136     115      120      125
137     ccc tgc cgc gcc gcc gag cgc ctc cag gtg ctg ctc acc tac cgc gtc      493
138     Pro Cys Arg Ala Ala Glu Arg Leu Gln Val Leu Leu Thr Tyr Arg Val
139     130      135      140
140     ggg gag gga ccc ggg gtt tgc tgg ttg gct ccc gag cag aca gca gga      541
141     Gly Glu Gly Pro Gly Val Cys Trp Leu Ala Pro Glu Gln Thr Ala Gly
142     145      150      155      160
143     aag aag aag ccc ttc gtg tac acc cag ggc cag gct gtc cta aac cgg      589
144     Lys Lys Lys Pro Phe Val Tyr Thr Gln Gly Gln Ala Val Leu Asn Arg
145     165      170      175
146     gcc ttc ttc cct tgc ttc gac acg cct gct gtt aaa tac aag tat tca      637

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147	Ala Phe Phe Pro Cys Phe Asp Thr Pro Ala Val Lys Tyr Lys Tyr Ser	
148	180 185 190	
149	gct ctt att gag gtc cca gat ggc ttc aca gct gtg atg agt gct agc	685
150	Ala Leu Ile Glu Val Pro Asp Gly Phe Thr Ala Val Met Ser Ala Ser	
151	195 200 205	
152	acc tgg gag aag aga ggt cca aat aag ttc ttc ttc cag atg tgt cag	733
153	Thr Trp Glu Lys Arg Gly Pro Asn Lys Phe Phe Phe Gln Met Cys Gln	
154	210 215 220	
155	ccc atc ccc tcc tat ctg ata gct ttg gcc atc gga gat ctg gtt tcg	781
156	Pro Ile Pro Ser Tyr Leu Ile Ala Leu Ala Ile Gly Asp Leu Val Ser	
157	225 230 235 240	
158	gct gaa gtt gga ccc agg agc cgg gtg tgg gct gag ccc tgc ctg att	829
159	Ala Glu Val Gly Pro Arg Ser Arg Val Trp Ala Glu Pro Cys Leu Ile	
160	245 250 255	
161	gat gct gcc aat gag gag tac aac ggg gtg ata gaa gaa ttt ttg gca	877
162	Asp Ala Ala Asn Glu Glu Tyr Asn Gly Val Ile Glu Glu Phe Leu Ala	
163	260 265 270	
164	aca gga gag aag ctt ttt gga cct tat gtt tgg gga agg tat gac ttg	925
165	Thr Gly Glu Lys Leu Phe Gly Pro Tyr Val Trp Gly Arg Tyr Asp Leu	
166	275 280 285	
167	ctc ttc atg cca ccg tcc ttt cca ttt gga gga atg gag aac cct tgt	973
168	Leu Phe Met Pro Pro Ser Phe Pro Phe Gly Gly Met Glu Asn Pro Cys	
169	290 295 300	
170	ctg acc ttt gtc acc ccc tgc ctg cta gct ggg gac cgc tcc ttg gca	1021
171	Leu Thr Phe Val Thr Pro Cys Leu Leu Ala Gly Asp Arg Ser Leu Ala	
172	305 310 315 320	
173	gat gtc atc atc cat gag atc tcc cac agt tgg ttt ggg aac ctg gtc	1069
174	Asp Val Ile Ile His Glu Ile Ser His Ser Trp Phe Gly Asn Leu Val	
175	325 330 335	
176	acc aac gcc aac tgg ggt gaa ttc tgg ctc aat gaa ggt ttc acc atg	1117
177	Thr Asn Ala Asn Trp Gly Glu Phe Trp Leu Asn Glu Gly Phe Thr Met	
178	340 345 350	
179	tac gcc cag agg agg atc tcc acc atc ctc ttt ggc gct gcg tac acc	1165
180	Tyr Ala Gln Arg Arg Ile Ser Thr Ile Leu Phe Gly Ala Ala Tyr Thr	
181	355 360 365	
182	tgc ttg gag gct gca acg ggg cgg gct ctg ctg cgt caa cac atg gac	1213
183	Cys Leu Glu Ala Ala Thr Gly Arg Ala Leu Leu Arg Gln His Met Asp	
184	370 375 380	
185	atc act gga gag gaa aac cca ctc aac aag ctc cgc gtg aag att gaa	1261
186	Ile Thr Gly Glu Glu Asn Pro Leu Asn Lys Leu Arg Val Lys Ile Glu	
187	385 390 395 400	
188	cca ggc gtt gac ccg gac gac acc tat aat gag acc ccc tac gag aaa	1309
189	Pro Gly Val Asp Pro Asp Asp Thr Tyr Asn Glu Thr Pro Tyr Glu Lys	
190	405 410 415	
191	ggg ttc tgc ttt gtc tca tac ctg gcc cac ttg gtg ggt gat cag gat	1357
192	Gly Phe Cys Phe Val Ser Tyr Leu Ala His Leu Val Gly Asp Gln Asp	
193	420 425 430	
194	cag ttt gac agt ttt ctc aag gcc tat gtg cat gaa ttc aaa ttc cga	1405
195	Gln Phe Asp Ser Phe Leu Lys Ala Tyr Val His Glu Phe Lys Phe Arg	

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196				435				440				445					
197	agc	atc	tta	gcc	gat	gac	ttt	ctg	gac	ttc	tac	ttg	gaa	tat	ttc	cct	1453
198	Ser	Ile	Leu	Ala	Asp	Asp	Phe	Leu	Asp	Phe	Tyr	Leu	Glu	Tyr	Phe	Pro	
199			450					455				460					
200	gag	ctt	aag	aaa	aag	aga	gtg	gat	atc	att	cca	ggg	ttt	gag	ttt	gat	1501
201	Glu	Leu	Lys	Lys	Lys	Arg	Val	Asp	Ile	Ile	Pro	Gly	Phe	Glu	Phe	Asp	
202	465						470					475				480	
203	cga	tg	ctg	aat	acc	ccc	ggc	tg	ccc	ccg	tac	ctc	cct	gat	ctc	tcc	1549
204	Arg	Trp	Leu	Asn	Thr	Pro	Gly	Trp	Pro	Pro	Tyr	Leu	Pro	Asp	Leu	Ser	
205					485					490					495		
206	cct	ggg	gac	tca	ctc	atg	aag	cct	gct	gaa	gag	cta	gcc	caa	ctg	tg	1597
207	Pro	Gly	Asp	Ser	Leu	Met	Lys	Pro	Ala	Glu	Glu	Leu	Ala	Gln	Leu	Trp	
208				500					505					510			
209	gca	gcc	gag	gag	ctg	gac	atg	aag	gcc	att	gaa	gcc	gtg	gcc	atc	tct	1645
210	Ala	Ala	Glu	Glu	Leu	Asp	Met	Lys	Ala	Ile	Glu	Ala	Val	Ala	Ile	Ser	
211			515					520					525				
212	ccc	tg	aag	acc	tac	cag	ctg	gtc	tac	ttc	ctg	gat	aag	atc	ctc	cag	1693
213	Pro	Trp	Lys	Thr	Tyr	Gln	Leu	Val	Tyr	Phe	Leu	Asp	Lys	Ile	Leu	Gln	
214		530					535					540					
215	aaa	tcc	cct	ctc	cct	cct	ggg	aat	gtg	aaa	aaa	ctt	gga	gac	aca	tac	1741
216	Lys	Ser	Pro	Leu	Pro	Pro	Gly	Asn	Val	Lys	Lys	Leu	Gly	Asp	Thr	Tyr	
217	545					550					555					560	
218	cca	agt	atc	tca	aat	gcc	cgg	aat	gca	gag	ctc	cgg	ctg	cga	tg	ggc	1789
219	Pro	Ser	Ile	Ser	Asn	Ala	Arg	Asn	Ala	Glu	Leu	Arg	Leu	Arg	Trp	Gly	
220				565						570					575		
221	caa	atc	gtc	ctt	aag	aac	gac	cac	cag	gaa	gat	ttc	tg	aaa	gtg	aag	1837
222	Gln	Ile	Val	Leu	Lys	Asn	Asp	His	Gln	Glu	Asp	Phe	Trp	Lys	Val	Lys	
223			580					585					590				
224	gag	ttc	ctg	cat	aac	cag	ggg	aag	cag	aag	tat	aca	ctt	ccg	ctg	tac	1885
225	Glu	Phe	Leu	His	Asn	Gln	Gly	Lys	Gln	Lys	Tyr	Thr	Leu	Pro	Leu	Tyr	
226			595					600					605				
227	cac	gca	atg	atg	ggg	ggc	agt	gag	gtg	gcc	cag	acc	ctc	gcc	aag	gag	1933
228	His	Ala	Met	Met	Gly	Gly	Ser	Glu	Val	Ala	Gln	Thr	Leu	Ala	Lys	Glu	
229		610					615					620					
230	act	ttt	gca	tcc	acc	gcc	tcc	cag	ctc	cac	agc	aat	gtt	gtc	aac	tat	1981
231	Thr	Phe	Ala	Ser	Thr	Ala	Ser	Gln	Leu	His	Ser	Asn	Val	Val	Asn	Tyr	
232	625					630											

**VERIFICATION SUMMARY**

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Input Set : N:\Crf3\RULE60\10056253.raw

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